

GeDiPNet Cluster 168 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See [scripts/build_cluster_enrichment.php](#) on [gedipnet.bicnirrh.res.in](#). Data as of: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 04:13:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Elastic fibre formation	Reactome	2	FBN2, LOXL4	18	52	25.66	2.691e-3	2.847e-2
Defective HK1 causes hexokinase deficiency (HK deficiency)	Reactome	1	HK1	1	52	230.96	4.330e-3	3.983e-2
Vitamins B6 activation to pyridoxal phosphate	Reactome	1	PDXK	3	52	76.99	1.293e-2	7.946e-2
Neomycin, kanamycin and gentamicin biosynthesis	KEGG	1	HK1	5	52	46.19	2.147e-2	1.071e-1
Activation of RAS in B cells	Reactome	1	RASGRP3	5	52	46.19	2.147e-2	1.071e-1
MET activates PTPN11	Reactome	1	GAB1	5	52	46.19	2.147e-2	1.071e-1
Caffeine metabolism	KEGG	1	XDH	6	52	38.49	2.570e-2	1.182e-1
Vitamin B6 metabolism	KEGG	1	PDXK	6	52	38.49	2.570e-2	1.182e-1
MET activates PI3K/AKT signaling	Reactome	1	GAB1	6	52	38.49	2.570e-2	1.182e-1
Signaling by FGFR3 fusions in cancer	Reactome	1	GAB1	10	52	23.10	4.248e-2	1.569e-1
MET receptor recycling	Reactome	1	GAB1	10	52	23.10	4.248e-2	1.569e-1
Signaling by FGFR4 in disease	Reactome	1	GAB1	11	52	21.00	4.663e-2	1.648e-1
MET activates RAP1 and RAC1	Reactome	1	GAB1	11	52	21.00	4.663e-2	1.648e-1
Ubiquinone and other terpenoid-quinone biosynthesis	KEGG	1	COQ2	12	52	19.25	5.076e-2	1.728e-1
Purine catabolism	Reactome	1	XDH	12	52	19.25	5.076e-2	1.728e-1